

SEQUENCE LISTING

<110> EINAT, Paz

SKALITER, Rami

FEINSTEIN, Elena

<120> SEQUENCES CHARACTERISTIC OF HYPOXIA-REGULATED GENE TRANSCRIPTION

<130> EINAT=4.1C

<150> US 09/383,096

<151> 1999-08-27

<150> US 09/138,109

<151> 1998-08-21

<150> US 60/098,158

<151> 1998-08-27

<150> US 60/132,684

<151> 1999-05-05

<160> 21

<170> PatentIn version 3.0

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<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (265)..(1575)

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<221> misc_feature

<223> "n" at every occurrence is unknown

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cgaagtcgct atttgcgtgc tgagcgcgct cgcagctcct ggaagtgttg ccgcctctcg 180
gtttcgetct cgctcgctgc gctcctagaa ggggcggccg cctccaggac tgaccagggc 240
caagtggcgc tcggcgggca ctac atg gcg gag ggt gaa ggg tac ttc gcc 291
Met Ala Glu Gly Glu Gly Tyr Phe Ala
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atg tct gag gac gag ctg gcc tgc agc ccc tac atc ccc cta ggc ggc 339
Met Ser Glu Asp Glu Leu Ala Cys Ser Pro Tyr Ile Pro Leu Gly Gly
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gac ttc ggc ggc ggc gac ttc ggc ggc ggc gac ttc ggc ggt ggc ggc 387
Asp Phe Gly Gly Gly Asp Phe Gly Gly Gly Asp Phe Gly Gly Gly Gly
30 35 40
agc ttc ggt ggg cat tgc ttg gac tat tgc gaa agc cct acg gcg cac 435
Ser Phe Gly Gly His Cys Leu Asp Tyr Cys Glu Ser Pro Thr Ala His
45 50 55
tgc aat gtg ctg aac tgg gag caa gtg cag cgg ctg gac ggc atc ctg 483
Cys Asn Val Leu Asn Trp Glu Gln Val Gln Arg Leu Asp Gly Ile Leu
60 65 70
agc gag acc att ccg att cac ggg cgc ggc aac ttc ccc acg ctc gag 531
Ser Glu Thr Ile Pro Ile His Gly Arg Gly Asn Phe Pro Thr Leu Glu
75 80 85
ctg cag ccg agc ctg atc gtg aag gtg gtg cgg cgg cgc ctg gcc gag 579
Leu Gln Pro Ser Leu Ile Val Lys Val Val Arg Arg Arg Leu Ala Glu
90 95 100 105

aag cgc att ggc gtc cgc gac gtg cgc ctc aac ggc tcg gca gcc agc Lys Arg Ile Gly Val Arg Asp Val Arg Leu Asn Gly Ser Ala Ala Ser	627
110 115 120	
cat gtc ctg cac cag gac agc ggc ctg ggc tac aag gac ctg gac ctc His Val Leu His Gln Asp Ser Gly Leu Gly Tyr Lys Asp Leu Asp Leu	675
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140 145 150	
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aaa gag aag atc aca cca ctc acg ctc aag gaa gct tat gtg cag aaa Lys Glu Lys Ile Thr Pro Leu Thr Leu Lys Glu Ala Tyr Val Gln Lys	819
170 175 180 185	
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190 195 200	
tca aac aac agt ggc aaa aat gtg gaa ctg aaa ttt gtg gat tcc ctc Ser Asn Asn Ser Gly Lys Asn Val Glu Leu Lys Phe Val Asp Ser Leu	915
205 210 215	
cgg agg cag ttt gaa ttc agt gta gat tct ttt caa atc aaa tta gac Arg Arg Gln Phe Glu Phe Ser Val Asp Ser Phe Gln Ile Lys Leu Asp	963
220 225 230	
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235 240 245	
ttt cac ccc aca ata atc ggg gag agc gtc tat ggc gat ttc cag gaa Phe His Pro Thr Ile Ile Gly Glu Ser Val Tyr Gly Asp Phe Gln Glu	1059
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gcc ttt gat cac ctt tgt aac aag atc att gcc acc agg aac cca gag Ala Phe Asp His Leu Cys Asn Lys Ile Ile Ala Thr Arg Asn Pro Glu	1107
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gaa atc cga ggg gga ggc ctg ctt aag tac tgc aac ctc ttg gtg agg Glu Ile Arg Gly Gly Gly Leu Leu Lys Tyr Cys Asn Leu Leu Val Arg	1155
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gct aat gtc act tgc tat tac cag cca gcc ccc tat gta gca gat gcc 1491
 Ala Asn Val Thr Cys Tyr Tyr Gln Pro Ala Pro Tyr Val Ala Asp Ala
 395 400 405

aac ttt agc aat tac tac att gca cag gtt cag cca gta ttc acg tgc 1539
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 410 415 420 425

cag caa cag acc tac tcc act tgg cta ccc tgc aat taagaatcat 1585
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<213> Homo sapiens

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<223> "n" at every occurrence is unknown

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Asp	Tyr	Cys	Glu	Ser	Pro	Thr	Ala	His	Cys	Asn	Val	Leu	Asn	Trp	Glu
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Gln	Val	Gln	Arg	Leu	Asp	Gly	Ile	Leu	Ser	Glu	Thr	Ile	Pro	Ile	His
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Gly	Arg	Gly	Asn	Phe	Pro	Thr	Leu	Glu	Leu	Gln	Pro	Ser	Leu	Ile	Val
			85						90					95	
Lys	Val	Val	Arg	Arg	Arg	Leu	Ala	Glu	Lys	Arg	Ile	Gly	Val	Arg	Asp
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Val	Arg	Leu	Asn	Gly	Ser	Ala	Ala	Ser	His	Val	Leu	His	Gln	Asp	Ser
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Gly	Leu	Gly	Tyr	Lys	Asp	Leu	Asp	Leu	Ile	Phe	Cys	Ala	Asp	Leu	Arg
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Gly	Glu	Gly	Glu	Phe	Gln	Thr	Val	Lys	Asp	Val	Val	Leu	Asp	Cys	Leu
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Leu	Asp	Phe	Leu	Pro	Glu	Gly	Val	Asn	Lys	Glu	Lys	Ile	Thr	Pro	Leu
				165					170						175
Thr	Leu	Lys	Glu	Ala	Tyr	Val	Gln	Lys	Met	Val	Lys	Val	Cys	Asn	Asp
			180					185					190		
Ser	Asp	Arg	Trp	Ser	Leu	Ile	Ser	Leu	Ser	Asn	Asn	Ser	Gly	Lys	Asn
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Val	Glu	Leu	Lys	Phe	Val	Asp	Ser	Leu	Arg	Arg	Gln	Phe	Glu	Phe	Ser
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			260					265					270		
Lys	Ile	Ile	Ala	Thr	Arg	Asn	Pro	Glu	Glu	Ile	Arg	Gly	Gly	Gly	Leu
	275						280					285			
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Leu His Gly Val Val Asn Glu Ser Ser Val Cys Leu Met Gly His Glu
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ccggcttcat tcgggcgtcc ctccgaaacc cactcgggtg cacgggtcgt cggcgagccg	300
cgaccgggtc ctggcgcgca cc atg atc gtg gcg gac tcc gag tgc cgc gca	352

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ggc	ccc	gga	gag	gag	cag	agg	gag	agc	cgg	gct	cgg	cga	ggc	cct	cga	448
Gly	Pro	Gly	Glu	Glu	Gln	Arg	Glu	Ser	Arg	Ala	Arg	Arg	Gly	Pro	Arg	
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Gly	Pro	Ser	Ala	Phe	Ile	Pro	Val	Glu	Glu	Val	Leu	Arg	Glu	Gly	Ala	
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Glu	Ser	Leu	Glu	Gln	His	Leu	Gly	Leu	Glu	Ala	Leu	Met	Ser	Ser	Gly	
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cga	gta	gac	aac	ctg	gca	gtg	gtg	atg	ggc	ctg	cac	cct	gac	tac	ttt	592
Arg	Val	Asp	Asn	Leu	Ala	Val	Val	Met	Gly	Leu	His	Pro	Asp	Tyr	Phe	
75				80				85				90				
acc	agc	ttc	tgg	cnc	ctg	cac	tac	ctg	ctg	ctg	cac	acg	gat	ggt	ccc	640
Thr	Ser	Phe	Trp	Xaa	Leu	His	Tyr	Leu	Leu	Leu	His	Thr	Asp	Gly	Pro	
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Leu	Ala	Ser	Ser	Trp	Arg	His	Tyr	Ile	Ala	Ile	Met	Ala	Ala	Ala	Arg	
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His	Gln	Cys	Ser	Tyr	Leu	Val	Gly	Ser	His	Met	Ala	Glu	Phe	Leu	Gln	
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Thr	Gly	Gly	Asp	Pro	Glu	Trp	Leu	Leu	Gly	Leu	His	Arg	Ala	Pro	Glu	
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aag	ctg	cgc	aaa	ctc	agc	gag	atc	aac	aag	ttg	ctg	gcg	cat	cgg	cca	832
Lys	Leu	Arg	Lys	Leu	Ser	Glu	Ile	Asn	Lys	Leu	Leu	Ala	His	Arg	Pro	
155				160				165				170				
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Trp	Leu	Ile	Thr	Lys	Glu	His	Ile	Gln	Ala	Leu	Leu	Lys	Thr	Gly	Glu	
175				180				185								
cac	act	tgg	tcc	ctg	gcc	gag	ctc	att	cag	gct	ctg	gtc	ctg	ctc	acc	928
His	Thr	Trp	Ser	Leu	Ala	Glu	Leu	Ile	Gln	Ala	Leu	Val	Leu	Leu	Thr	
190				195				200								
cac	tgc	cac	tcg	ctc	tcc	tcc	ttc	gtg	ttt	ggc	tgt	ggc	atc	ctc	cct	976
His	Cys	His	Ser	Leu	Ser	Ser	Phe	Val	Phe	Gly	Cys	Gly	Ile	Leu	Pro	
205				210				215								
gag	ggg	gat	gca	gat	ggc	agc	cct	gcc	ccc	cag	gca	cct	aca	ccc	cct	1024

Glu Gly Asp Ala Asp Gly Ser Pro Ala Pro Gln Ala Pro Thr Pro Pro	
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Ser Glu Gln Ser Ser Pro Pro Ser Arg Asp Pro Leu Asn Asn Ser Gly	
235 240 245 250	
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Gly Phe Glu Ser Ala Arg Asp Val Glu Ala Leu Met Glu Arg Met Gln	
255 260 265	
cag ctg cag gag agc ctg ctg cgg gat gag ggg acg tcc cag gag gag	1168
Gln Leu Gln Glu Ser Leu Leu Arg Asp Glu Gly Thr Ser Gln Glu Glu	
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atg gag agc cgc ttt gag ctg gag aag tca gag agc ctg ctg gtg acc	1216
Met Glu Ser Arg Phe Glu Leu Glu Lys Ser Glu Ser Leu Leu Val Thr	
285 290 295	
ccc tca gct gac atc ctg gag ccc tct cca cac cca gac atg ctg tgc	1264
Pro Ser Ala Asp Ile Leu Glu Pro Ser Pro His Pro Asp Met Leu Cys	
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Phe Val Glu Asp Pro Thr Phe Gly Tyr Glu Asp Phe Thr Arg Arg Gly	
315 320 325 330	
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Ala Gln Ala Pro Pro Thr Phe Arg Ala Gln Asp Tyr Thr Trp Glu Asp	
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His Gly Tyr Ser Leu Ile Gln Arg Leu Tyr Pro Glu Gly Gly Gln Leu	
350 355 360	
ctg gat gag aag ttc cag gca gcc tat agc ctc acc tac aat acc atc	1456
Leu Asp Glu Lys Phe Gln Ala Ala Tyr Ser Leu Thr Tyr Asn Thr Ile	
365 370 375	
gcc atg cac agt ggt gtg gac acc tcc gtg ctc cgc agg gcc atc tgg	1504
Ala Met His Ser Gly Val Asp Thr Ser Val Leu Arg Arg Ala Ile Trp	
380 385 390	
aac tat atc cac tgc gtc ttt ggc atc aga tat gat gac tat gat tat	1552
Asn Tyr Ile His Cys Val Phe Gly Ile Arg Tyr Asp Asp Tyr Asp Tyr	
395 400 405 410	
ggg gag gtg aac cag ctc ctg gag cgg aac ctc aag gtc tat atc aag	1600
Gly Glu Val Asn Gln Leu Leu Glu Arg Asn Leu Lys Val Tyr Ile Lys	
415 420 425	
aca gtg gcc tgc tac cca gag aag acc acc cga aga atg tac aac ctc	1648
Thr Val Ala Cys Tyr Pro Glu Lys Thr Thr Arg Arg Met Tyr Asn Leu	
430 435 440	
ttc tgg agg cac ttc cgc cac tca gag aag gtc cac gtg aac ttg ctg	1696

Phe Trp Arg His Phe Arg His Ser Glu Lys Val His Val Asn Leu Leu	
445 450 455	
ctc ctg gag gcg cgc atg caa gcc gct ctg ctg tac gcc ctc cgt gcc	1744
Leu Leu Glu Ala Arg Met Gln Ala Ala Leu Leu Tyr Ala Leu Arg Ala	
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Ile Thr Arg Tyr Met Thr	
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<211> 480

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> "n" at every occurrence is unknown

<400> 4

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Arg Glu Ser Arg Ala Arg Arg Gly Pro Arg Gly Pro Ser Ala Phe Ile
35 40 45

Pro Val Glu Glu Val Leu Arg Glu Gly Ala Glu Ser Leu Glu Gln His
50 55 60

Leu Gly Leu Glu Ala Leu Met Ser Ser Gly Arg Val Asp Asn Leu Ala
65 70 75 80

Val Val Met Gly Leu His Pro Asp Tyr Phe Thr Ser Phe Trp Xaa Leu
85 90 95

His Tyr Leu Leu Leu His Thr Asp Gly Pro Leu Ala Ser Ser Trp Arg
100 105 110

His Tyr Ile Ala Ile Met Ala Ala Ala Arg His Gln Cys Ser Tyr Leu
115 120 125

Val Gly Ser His Met Ala Glu Phe Leu Gln Thr Gly Gly Asp Pro Glu
130 135 140

Trp Leu Leu Gly Leu His Arg Ala Pro Glu Lys Leu Arg Lys Leu Ser
145 150 155 160

Glu Ile Asn Lys Leu Leu Ala His Arg Pro Trp Leu Ile Thr Lys Glu
 165 170 175
 His Ile Gln Ala Leu Leu Lys Thr Gly Glu His Thr Trp Ser Leu Ala
 180 185 190
 Glu Leu Ile Gln Ala Leu Val Leu Leu Thr His Cys His Ser Leu Ser
 195 200 205
 Ser Phe Val Phe Gly Cys Gly Ile Leu Pro Glu Gly Asp Ala Asp Gly
 210 215 220
 Ser Pro Ala Pro Gln Ala Pro Thr Pro Pro Ser Glu Gln Ser Ser Pro
 225 230 235 240
 Pro Ser Arg Asp Pro Leu Asn Asn Ser Gly Gly Phe Glu Ser Ala Arg
 245 250 255
 Asp Val Glu Ala Leu Met Glu Arg Met Gln Gln Leu Gln Glu Ser Leu
 260 265 270
 Leu Arg Asp Glu Gly Thr Ser Gln Glu Glu Met Glu Ser Arg Phe Glu
 275 280 285
 Leu Glu Lys Ser Glu Ser Leu Leu Val Thr Pro Ser Ala Asp Ile Leu
 290 295 300
 Glu Pro Ser Pro His Pro Asp Met Leu Cys Phe Val Glu Asp Pro Thr
 305 310 315 320
 Phe Gly Tyr Glu Asp Phe Thr Arg Arg Gly Ala Gln Ala Pro Pro Thr
 325 330 335
 Phe Arg Ala Gln Asp Tyr Thr Trp Glu Asp His Gly Tyr Ser Leu Ile
 340 345 350
 Gln Arg Leu Tyr Pro Glu Gly Gly Gln Leu Leu Asp Glu Lys Phe Gln
 355 360 365
 Ala Ala Tyr Ser Leu Thr Tyr Asn Thr Ile Ala Met His Ser Gly Val
 370 375 380
 Asp Thr Ser Val Leu Arg Arg Ala Ile Trp Asn Tyr Ile His Cys Val
 385 390 395 400
 Phe Gly Ile Arg Tyr Asp Asp Tyr Asp Tyr Gly Glu Val Asn Gln Leu
 405 410 415
 Leu Glu Arg Asn Leu Lys Val Tyr Ile Lys Thr Val Ala Cys Tyr Pro
 420 425 430
 Glu Lys Thr Thr Arg Arg Met Tyr Asn Leu Phe Trp Arg His Phe Arg
 435 440 445
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465

470

475

480

<210> 5

<211> 4138

<212> DNA

<213> Homo sapiens

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<211> 1303

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> "n" at every occurrence is unknown

<400> 6

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<210> 7

<211> 244

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> "Xaa" at position 118 is unknown

<400> 7

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Gln Cys Gly Lys Thr Ala Leu Leu His Val Phe Ala Lys Asp Cys Phe
35 40 45
Pro Glu Asn Tyr Val Pro Thr Val Phe Glu Asn Tyr Thr Ala Ser Phe
50 55 60
Glu Ile Asp Thr Gln Arg Ile Glu Leu Ser Leu Trp Asp Thr Ser Gly
65 70 75 80
Ser Pro Tyr Tyr Asp Asn Val Arg Pro Leu Ser Tyr Pro Asp Ser Asp
85 90 95
Ala Val Leu Ile Cys Phe Asp Ile Ser Arg Pro Glu Thr Leu Asp Ser
100 105 110
Val Leu Lys Lys Trp Xaa Gly Glu Ile Gln Glu Phe Cys Pro Asn Thr
115 120 125
Lys Met Leu Leu Val Gly Cys Lys Ser Asp Leu Arg Thr Asp Val Ser
130 135 140
Thr Leu Val Glu Leu Ser Asn His Arg Gln Thr Pro Val Ser Tyr Asp
145 150 155 160
Gln Gly Ala Asn Met Ala Lys Gln Ile Gly Ala Ala Thr Tyr Ile Glu
165 170 175
Cys Ser Ala Leu Gln Ser Glu Asn Ser Val Arg Asp Ile Phe His Val
180 185 190
Ala Thr Leu Ala Cys Val Asn Lys Thr Asn Lys Asn Val Lys Arg Asn
195 200 205
Lys Ser Gln Arg Ala Thr Lys Arg Ile Ser His Met Pro Ser Arg Pro
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<210> 8

<211> 2479

<212> DNA

<213> Rattus rattus

<220>

<221> CDS

<222> (1)..(2274)

<400> 8

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Leu	His	Pro	Trp	Asn	Pro	Cys	Leu	Gly	Ala	Asp	Ser	Glu	Lys	Pro	Ser	
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agc	atc	ccc	aca	gat	aaa	tta	tta	gtc	ata	act	gta	gca	aca	aaa	gaa	144
Ser	Ile	Pro	Thr	Asp	Lys	Leu	Leu	Val	Ile	Thr	Val	Ala	Thr	Lys	Glu	
		35				40					45					

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	50					55					60					

act	gtg	aag	gtc	ctt	ggg	caa	gga	gaa	gaa	tgg	aga	ggg	ggg	gat	gga	240
Thr	Val	Lys	Val	Leu	Gly	Gln	Gly	Glu	Glu	Trp	Arg	Gly	Gly	Asp	Gly	
65				70				75						80		

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Ile	Asn	Ser	Ile	Gly	Gly	Gly	Gln	Lys	Val	Arg	Leu	Met	Lys	Glu	Val	
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atg	gaa	cac	tat	gct	gat	caa	gat	gat	ctg	gtt	gtc	atg	ttt	act	gaa	336
Met	Glu	His	Tyr	Ala	Asp	Gln	Asp	Asp	Leu	Val	Val	Met	Phe	Thr	Glu	
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Cys	Phe	Asp	Val	Ile	Phe	Ala	Gly	Gly	Pro	Glu	Glu	Val	Leu	Lys	Lys	
	115					120						125				

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Phe	Gln	Lys	Ala	Asn	His	Lys	Val	Val	Phe	Ala	Ala	Asp	Gly	Ile	Leu	
	130					135				140						

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Trp	Pro	Asp	Lys	Arg	Leu	Ala	Asp	Lys	Tyr	Pro	Val	Val	His	Ile	Gly	
145					150					155					160	

aaa	cgc	tat	ctg	aat	tca	gga	gga	ttt	att	ggc	tat	gct	cca	tat	gtc	528
Lys	Arg	Tyr	Leu	Asn	Ser	Gly	Gly	Phe	Ile	Gly	Tyr	Ala	Pro	Tyr	Val	

165	170	175	
aac cgt ata gtt caa caa tgg aat ctc cag gat aat gat gat gat cag Asn Arg Ile Val Gln Gln Trp Asn Leu Gln Asp Asn Asp Asp Asp Gln 180 185 190			576
ctc ttt tac act aaa gtt tac att gat cca ctg aaa agg gaa gct att Leu Phe Tyr Thr Lys Val Tyr Ile Asp Pro Leu Lys Arg Glu Ala Ile 195 200 205			624
aac atc aca ttg gat cac aaa tgc aaa att ttc cag acc tta aat gga Asn Ile Thr Leu Asp His Lys Cys Lys Ile Phe Gln Thr Leu Asn Gly 210 215 220			672
gct gta gat gaa gtt gtt tta aaa ttt gaa aat ggc aaa gcc aga gct Ala Val Asp Glu Val Val Leu Lys Phe Glu Asn Gly Lys Ala Arg Ala 225 230 235 240			720
aag aat aca ttt tat gaa aca tta cca gtg gca att aat gga aat gga Lys Asn Thr Phe Tyr Glu Thr Leu Pro Val Ala Ile Asn Gly Asn Gly 245 250 255			768
ccc acc aag att ctc ctg aat tat ttt gga aac tat gta ccc aat tca Pro Thr Lys Ile Leu Leu Asn Tyr Phe Gly Asn Tyr Val Pro Asn Ser 260 265 270			816
tgg aca cag gat aat ggc tgc act ctt tgt gaa ttc gat aca gtc gac Trp Thr Gln Asp Asn Gly Cys Thr Leu Cys Glu Phe Asp Thr Val Asp 275 280 285			864
ttg tct gca gta gat gtc cat cca aac gta tca ata ggt gtt ttt att Leu Ser Ala Val Asp Val His Pro Asn Val Ser Ile Gly Val Phe Ile 290 295 300			912
gag caa cca acc cct ttt cta cct cgg ttt ctg gac ata ttg ttg aca Glu Gln Pro Thr Pro Phe Leu Pro Arg Phe Leu Asp Ile Leu Leu Thr 305 310 315 320			960
ctg gat tac cca aaa gaa gca ctt aaa ctt ttt att cat aac aaa gaa Leu Asp Tyr Pro Lys Glu Ala Leu Lys Leu Phe Ile His Asn Lys Glu 325 330 335			1008
gtt tat cat gaa aag gac atc aag gta ttt ttt gat aaa gct aag cat Val Tyr His Glu Lys Asp Ile Lys Val Phe Phe Asp Lys Ala Lys His 340 345 350			1056
gaa atc aaa act ata aaa ata gta gga cca gaa gaa aat cta agt caa Glu Ile Lys Thr Ile Lys Ile Val Gly Pro Glu Glu Asn Leu Ser Gln 355 360 365			1104
gcg gaa gcc aga aac atg gga atg gac ttt tgc cgt cag gat gaa aag Ala Glu Ala Arg Asn Met Gly Met Asp Phe Cys Arg Gln Asp Glu Lys 370 375 380			1152
tgt gat tat tac ttt agt gtg gat gca gat gtt gtt ttg aca aat cca Cys Asp Tyr Tyr Phe Ser Val Asp Ala Asp Val Val Leu Thr Asn Pro			1200

385	390	395	400	
agg act tta aaa att ttg att gaa caa aac aga aag atc att gct cct				1248
Arg Thr Leu Lys Ile Leu Ile Glu Gln Asn Arg Lys Ile Ile Ala Pro	405	410	415	
ctt gta act cgt cat gga aag ctg tgg tcc aat ttc tgg gga gca ttg				1296
Leu Val Thr Arg His Gly Lys Leu Trp Ser Asn Phe Trp Gly Ala Leu	420	425	430	
agt cct gat gga tac tat gca cga tct gaa gat tat gtg gat att gtt				1344
Ser Pro Asp Gly Tyr Tyr Ala Arg Ser Glu Asp Tyr Val Asp Ile Val	435	440	445	
caa ggg aat aga gta gga gta tgg aat gtc cca tat atg gct aat gtg				1392
Gln Gly Asn Arg Val Gly Val Trp Asn Val Pro Tyr Met Ala Asn Val	450	455	460	
tac tta att aaa gga aag aca ctc cga tca gag atg aat gaa agg aac				1440
Tyr Leu Ile Lys Gly Lys Thr Leu Arg Ser Glu Met Asn Glu Arg Asn	465	470	475	480
tat ttt gtt cgt gat aaa ctg gat cct gat atg gct ctt tgc cga aat				1488
Tyr Phe Val Arg Asp Lys Leu Asp Pro Asp Met Ala Leu Cys Arg Asn	485	490	495	
gct aga gaa atg act tta caa agg gaa aaa gac tcc cct act ccg gaa				1536
Ala Arg Glu Met Thr Leu Gln Arg Glu Lys Asp Ser Pro Thr Pro Glu	500	505	510	
aca ttc caa atg ctc agc ccc cca aag ggt gta ttt atg tac att tct				1584
Thr Phe Gln Met Leu Ser Pro Pro Lys Gly Val Phe Met Tyr Ile Ser	515	520	525	
aat aga cat gaa ttt gga agg cta tta tcc act gct aat tac aat act				1632
Asn Arg His Glu Phe Gly Arg Leu Leu Ser Thr Ala Asn Tyr Asn Thr	530	535	540	
tcc cat tat aac aat gac ctc tgg cag att ttt gaa aat cct gtg gac				1680
Ser His Tyr Asn Asn Asp Leu Trp Gln Ile Phe Glu Asn Pro Val Asp	545	550	555	560
tgg aag gaa aag tat ata aac cgt gat tat tca aag att ttc act gaa				1728
Trp Lys Glu Lys Tyr Ile Asn Arg Asp Tyr Ser Lys Ile Phe Thr Glu	565	570	575	
aat ata gtt gaa cag ccc tgt cca gat gtc ttt tgg ttc ccc ata ttt				1776
Asn Ile Val Glu Gln Pro Cys Pro Asp Val Phe Trp Phe Pro Ile Phe	580	585	590	
tct gaa aaa gcc tgt gat gaa ttg gta gaa gaa atg gaa cat tac ggc				1824
Ser Glu Lys Ala Cys Asp Glu Leu Val Glu Glu Met Glu His Tyr Gly	595	600	605	
aaa tgg tct ggg gga aaa cat cat gat agc cgt ata tct ggt ggt tat				1872
Lys Trp Ser Gly Gly Lys His His Asp Ser Arg Ile Ser Gly Gly Tyr				

610	615	620	
gaa aat gtc cca act gat gat atc cac atg aag caa gtt gat ctg gag			1920
Glu Asn Val Pro Thr Asp Asp Ile His Met Lys Gln Val Asp Leu Glu			
625	630	635	640
aat gta tgg ctt cat ttt atc cgg gag ttc att gca cca gtt aca ctg			1968
Asn Val Trp Leu His Phe Ile Arg Glu Phe Ile Ala Pro Val Thr Leu			
645	650		655
aag gtc ttt gca ggc tat tat acg aag gga ttt gca cta ctg aat ttt			2016
Lys Val Phe Ala Gly Tyr Tyr Thr Lys Gly Phe Ala Leu Leu Asn Phe			
660	665		670
gta gta aaa tac tcc cct gaa cga cag cgt tct ctt cgt cct cat cat			2064
Val Val Lys Tyr Ser Pro Glu Arg Gln Arg Ser Leu Arg Pro His His			
675	680		685
gat gct tct aca ttt acc ata aac att gca ctt aat aac gtg gga gaa			2112
Asp Ala Ser Thr Phe Thr Ile Asn Ile Ala Leu Asn Asn Val Gly Glu			
690	695	700	

Met	Gly	Gly	Cys	Thr	Val	Lys	Pro	Gln	Leu	Leu	Leu	Leu	Ala	Leu	Val	1	5	10	15
Leu	His	Pro	Trp	Asn	Pro	Cys	Leu	Gly	Ala	Asp	Ser	Glu	Lys	Pro	Ser	20	25	30	
Ser	Ile	Pro	Thr	Asp	Lys	Leu	Leu	Val	Ile	Thr	Val	Ala	Thr	Lys	Glu	35	40	45	
Ser	Asp	Gly	Phe	His	Arg	Phe	Met	Gln	Ser	Ala	Lys	Tyr	Phe	Asn	Tyr	50	55	60	
Thr	Val	Lys	Val	Leu	Gly	Gln	Gly	Glu	Glu	Trp	Arg	Gly	Gly	Asp	Gly	65	70	75	80
Ile	Asn	Ser	Ile	Gly	Gly	Gly	Gln	Lys	Val	Arg	Leu	Met	Lys	Glu	Val	85	90	95	
Met	Glu	His	Tyr	Ala	Asp	Gln	Asp	Asp	Leu	Val	Val	Met	Phe	Thr	Glu	100	105	110	
Cys	Phe	Asp	Val	Ile	Phe	Ala	Gly	Gly	Pro	Glu	Glu	Val	Leu	Lys	Lys	115	120	125	
Phe	Gln	Lys	Ala	Asn	His	Lys	Val	Val	Phe	Ala	Ala	Asp	Gly	Ile	Leu	130	135	140	
Trp	Pro	Asp	Lys	Arg	Leu	Ala	Asp	Lys	Tyr	Pro	Val	Val	His	Ile	Gly	145	150	155	160
Lys	Arg	Tyr	Leu	Asn	Ser	Gly	Gly	Phe	Ile	Gly	Tyr	Ala	Pro	Tyr	Val	165	170	175	
Asn	Arg	Ile	Val	Gln	Gln	Trp	Asn	Leu	Gln	Asp	Asn	Asp	Asp	Asp	Gln	180	185	190	
Leu	Phe	Tyr	Thr	Lys	Val	Tyr	Ile	Asp	Pro	Leu	Lys	Arg	Glu	Ala	Ile	195	200	205	
Asn	Ile	Thr	Leu	Asp	His	Lys	Cys	Lys	Ile	Phe	Gln	Thr	Leu	Asn	Gly	210	215	220	
Ala	Val	Asp	Glu	Val	Val	Leu	Lys	Phe	Glu	Asn	Gly	Lys	Ala	Arg	Ala	225	230	235	240
Lys	Asn	Thr	Phe	Tyr	Glu	Thr	Leu	Pro	Val	Ala	Ile	Asn	Gly	Asn	Gly	245	250	255	
Pro	Thr	Lys	Ile	Leu	Leu	Asn	Tyr	Phe	Gly	Asn	Tyr	Val	Pro	Asn	Ser	260	265	270	
Trp	Thr	Gln	Asp	Asn	Gly	Cys	Thr	Leu	Cys	Glu	Phe	Asp	Thr	Val	Asp	275	280	285	
Leu	Ser	Ala	Val	Asp	Val	His	Pro	Asn	Val	Ser	Ile	Gly	Val	Phe	Ile	290	295	300	

Glu Gln Pro Thr Pro Phe Leu Pro Arg Phe Leu Asp Ile Leu Leu Thr
 305 310 315 320
 Leu Asp Tyr Pro Lys Glu Ala Leu Lys Leu Phe Ile His Asn Lys Glu
 325 330 335
 Val Tyr His Glu Lys Asp Ile Lys Val Phe Phe Asp Lys Ala Lys His
 340 345 350
 Glu Ile Lys Thr Ile Lys Ile Val Gly Pro Glu Glu Asn Leu Ser Gln
 355 360 365
 Ala Glu Ala Arg Asn Met Gly Met Asp Phe Cys Arg Gln Asp Glu Lys
 370 375 380
 Cys Asp Tyr Tyr Phe Ser Val Asp Ala Asp Val Val Leu Thr Asn Pro
 385 390 395 400
 Arg Thr Leu Lys Ile Leu Ile Glu Gln Asn Arg Lys Ile Ile Ala Pro
 405 410 415
 Leu Val Thr Arg His Gly Lys Leu Trp Ser Asn Phe Trp Gly Ala Leu
 420 425 430
 Ser Pro Asp Gly Tyr Tyr Ala Arg Ser Glu Asp Tyr Val Asp Ile Val
 435 440 445
 Gln Gly Asn Arg Val Gly Val Trp Asn Val Pro Tyr Met Ala Asn Val
 450 455 460
 Tyr Leu Ile Lys Gly Lys Thr Leu Arg Ser Glu Met Asn Glu Arg Asn
 465 470 475 480
 Tyr Phe Val Arg Asp Lys Leu Asp Pro Asp Met Ala Leu Cys Arg Asn
 485 490 495
 Ala Arg Glu Met Thr Leu Gln Arg Glu Lys Asp Ser Pro Thr Pro Glu
 500 505 510
 Thr Phe Gln Met Leu Ser Pro Pro Lys Gly Val Phe Met Tyr Ile Ser
 515 520 525
 Asn Arg His Glu Phe Gly Arg Leu Leu Ser Thr Ala Asn Tyr Asn Thr
 530 535 540
 Ser His Tyr Asn Asn Asp Leu Trp Gln Ile Phe Glu Asn Pro Val Asp
 545 550 555 560
 Trp Lys Glu Lys Tyr Ile Asn Arg Asp Tyr Ser Lys Ile Phe Thr Glu
 565 570 575
 Asn Ile Val Glu Gln Pro Cys Pro Asp Val Phe Trp Phe Pro Ile Phe
 580 585 590
 Ser Glu Lys Ala Cys Asp Glu Leu Val Glu Glu Met Glu His Tyr Gly
 595 600 605

Lys Trp Ser Gly Gly Lys His His Asp Ser Arg Ile Ser Gly Gly Tyr
 610 615 620
 Glu Asn Val Pro Thr Asp Asp Ile His Met Lys Gln Val Asp Leu Glu
 625 630 635 640
 Asn Val Trp Leu His Phe Ile Arg Glu Phe Ile Ala Pro Val Thr Leu
 645 650 655
 Lys Val Phe Ala Gly Tyr Tyr Thr Lys Gly Phe Ala Leu Leu Asn Phe
 660 665 670
 Val Val Lys Tyr Ser Pro Glu Arg Gln Arg Ser Leu Arg Pro His His
 675 680 685
 Asp Ala Ser Thr Phe Thr Ile Asn Ile Ala Leu Asn Asn Val Gly Glu
 690 695 700
 Asp Phe Gln Gly Gly Gly Cys Lys Phe Leu Arg Tyr Asn Cys Ser Ile
 705 710 715 720
 Glu Ser Pro Arg Lys Gly Trp Ser Phe Met His Pro Gly Arg Leu Thr
 725 730 735
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 740 745 750
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ctc cac ccc tgg aat ccc tgt ctg ggt gcg gac tcg gag aag ccc tcg	96
Leu His Pro Trp Asn Pro Cys Leu Gly Ala Asp Ser Glu Lys Pro Ser	
20 25 30	

agc atc ccc aca gat aaa tta tta gtc ata act gta gca aca aaa gaa	144
Ser Ile Pro Thr Asp Lys Leu Val Ile Thr Val Ala Thr Lys Glu	
35 40 45	
agt gat gga ttc cat cga ttt atg cag tca gcc aaa tat ttc aat tat	192
Ser Asp Gly Phe His Arg Phe Met Gln Ser Ala Lys Tyr Phe Asn Tyr	
50 55 60	
act gtg aag gtc ctt ggt caa gga gaa gaa tgg aga ggt ggt gat gga	240
Thr Val Lys Val Leu Gly Gln Gly Glu Glu Trp Arg Gly Gly Asp Gly	
65 70 75 80	
att aat agt att gga ggg ggc cag aaa gtg aga tta atg aaa gaa gtc	288
Ile Asn Ser Ile Gly Gly Gly Gln Lys Val Arg Leu Met Lys Glu Val	
85 90 95	
atg gaa cac tat gct gat caa gat gat ctg gtt gtc atg ttt act gaa	336
Met Glu His Tyr Ala Asp Gln Asp Asp Leu Val Val Met Phe Thr Glu	
100 105 110	
tgc ttt gat gtc ata ttt gct ggt ggt cca gaa gaa gtt cta aaa aaa	384
Cys Phe Asp Val Ile Phe Ala Gly Gly Pro Glu Glu Val Leu Lys Lys	
115 120 125	
ttc caa aag gca aac cac aaa gtg gtc ttt gca gca gat gga att ttg	432
Phe Gln Lys Ala Asn His Lys Val Val Phe Ala Ala Asp Gly Ile Leu	
130 135 140	
tgg cca gat aaa aga cta gca gac aag tat cct gtt gtg cac att ggg	480
Trp Pro Asp Lys Arg Leu Ala Asp Lys Tyr Pro Val Val His Ile Gly	
145 150 155 160	
aaa cgc tat ctg aat tca gga gga ttt att ggc tat gct cca tat gtc	528
Lys Arg Tyr Leu Asn Ser Gly Gly Phe Ile Gly Tyr Ala Pro Tyr Val	
165 170 175	
aac cgt ata gtt caa caa tgg aat ctc cag gat aat gat gat gat cag	576
Asn Arg Ile Val Gln Gln Trp Asn Leu Gln Asp Asn Asp Asp Asp Gln	
180 185 190	
ctc ttt tac act aaa gtt tac att gat cca ctg aaa agg gaa gct att	624
Leu Phe Tyr Thr Lys Val Tyr Ile Asp Pro Leu Lys Arg Glu Ala Ile	
195 200 205	
aac atc aca ttg gat cac aaa tgc aaa att ttc cag acc tta aat gga	672
Asn Ile Thr Leu Asp His Lys Cys Lys Ile Phe Gln Thr Leu Asn Gly	
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gct gta gat gaa gtt gtt tta aaa ttt gaa aat ggc aaa gcc aga gct	720
Ala Val Asp Glu Val Val Leu Lys Phe Glu Asn Gly Lys Ala Arg Ala	
225 230 235 240	
aag aat aca ttt tat gaa aca tta cca gtg gca att aat gga aat gga	768
Lys Asn Thr Phe Tyr Glu Thr Leu Pro Val Ala Ile Asn Gly Asn Gly	
245 250 255	

ccc acc aag att ctc ctg aat tat ttt gga aac tat gta ccc aat tca	816
Pro Thr Lys Ile Leu Leu Asn Tyr Phe Gly Asn Tyr Val Pro Asn Ser	
260 265 270	
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Trp Thr Gln Asp Asn Gly Cys Thr Leu Cys Glu Phe Asp Thr Val Asp	
275 280 285	
ttgtt tct gca gta gat gtc cat cca aac gta tca ata ggt gtt ttt att	912
Leu Ser Ala Val Asp Val His Pro Asn Val Ser Ile Gly Val Phe Ile	
290 295 300	
gag caa cca acc cct ttt cta cct cgg ttt ctg gac ata ttg ttg aca	960
Glu Gln Pro Thr Pro Phe Leu Pro Arg Phe Leu Asp Ile Leu Leu Thr	
305 310 315 320	
ctg gat tac cca aaa gaa gca ctt aaa ctt ttt att cat aac aaa gaa	1008
Leu Asp Tyr Pro Lys Glu Ala Leu Lys Leu Phe Ile His Asn Lys Glu	
325 330 335	
gtt tat cat gaa aag gac atc aag gta ttt ttt gat aaa gct aag cat	1056
Val Tyr His Glu Lys Asp Ile Lys Val Phe Phe Asp Lys Ala Lys His	
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gaa atc aaa act ata aaa ata gta gga cca gaa gaa aat cta agt caa	1104
Glu Ile Lys Thr Ile Lys Ile Val Gly Pro Glu Glu Asn Leu Ser Gln	
355 360 365	
gcg gaa gcc aga aac atg gga atg gac ttt tgc cgt cag gat gaa aag	1152
Ala Glu Ala Arg Asn Met Gly Met Asp Phe Cys Arg Gln Asp Glu Lys	
370 375 380	
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Cys Asp Tyr Tyr Phe Ser Val Asp Ala Asp Val Val Leu Thr Asn Pro	
385 390 395 400	
agg act tta aaa att ttg att gaa caa aac aga aag atc att gct cct	1248
Arg Thr Leu Lys Ile Leu Ile Glu Gln Asn Arg Lys Ile Ile Ala Pro	
405 410 415	
ctt gta act cgt cat gga aag ctg tgg tcc aat ttc tgg gga gca ttg	1296
Leu Val Thr Arg His Gly Lys Leu Trp Ser Asn Phe Trp Gly Ala Leu	
420 425 430	
agt cct gat gga tac tat gca cga tct gaa gat tat gtg gat att gtt	1344
Ser Pro Asp Gly Tyr Tyr Ala Arg Ser Glu Asp Tyr Val Asp Ile Val	
435 440 445	
caa ggg aat aga gta gga gta tgg aat gtc cca tat atg gct aat gtg	1392
Gln Gly Asn Arg Val Gly Val Trp Asn Val Pro Tyr Met Ala Asn Val	
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Tyr Leu Ile Lys Gly Lys Thr Leu Arg Ser Glu Met Asn Glu Arg Asn	
465 470 475 480	

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Tyr Phe Val Arg Asp Lys Leu Asp Pro Asp Met Ala Leu Cys Arg Asn	
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gct aga gaa atg act tta caa agg gaa aaa gac tcc cct act ccg gaa	1536
Ala Arg Glu Met Thr Leu Gln Arg Glu Lys Asp Ser Pro Thr Pro Glu	
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Thr Phe Gln Met Leu Ser Pro Pro Lys Gly Val Phe Met Tyr Ile Ser	
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Asn Arg His Glu Phe Gly Arg Leu Leu Ser Thr Ala Asn Tyr Asn Thr	
530 535 540	
tcc cat tat aac aat gac ctc tgg cag att ttt gaa aat cct gtg gac	1680
Ser His Tyr Asn Asn Asp Leu Trp Gln Ile Phe Glu Asn Pro Val Asp	
545 550 555 560	
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Trp Lys Glu Lys Tyr Ile Asn Arg Asp Tyr Ser Lys Ile Phe Thr Glu	
565 570 575	
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Asn Ile Val Glu Gln Pro Cys Pro Asp Val Phe Trp Phe Pro Ile Phe	
580 585 590	
tct gaa aaa gcc tgt gat gaa ttg gta gaa gaa atg gaa cat tac ggc	1824
Ser Glu Lys Ala Cys Asp Glu Leu Val Glu Glu Met Glu His Tyr Gly	
595 600 605	
aaa tgg tct ggg gga aaa cat cat gat agc cgt ata tct ggt ggt tat	1872
Lys Trp Ser Gly Gly Lys His His Asp Ser Arg Ile Ser Gly Gly Tyr	
610 615 620	
gaa aat gtc cca act gat gat atc cac atg aag caa gtt gat ctg gag	1920
Glu Asn Val Pro Thr Asp Asp Ile His Met Lys Gln Val Asp Leu Glu	
625 630 635 640	
aat gta tgg ctt cat ttt atc cgg gag ttc att gca cca gtt aca ctg	1968
Asn Val Trp Leu His Phe Ile Arg Glu Phe Ile Ala Pro Val Thr Leu	
645 650 655	
aag gtc ttt gca ggc tat tat acg aag gga ttt gca cta ctg aat ttt	2016
Lys Val Phe Ala Gly Tyr Tyr Thr Lys Gly Phe Ala Leu Leu Asn Phe	
660 665 670	
gta gta aaa tac tcc cct gaa cga cag cgt tct ctt cgt cct cat cat	2064
Val Val Lys Tyr Ser Pro Glu Arg Gln Arg Ser Leu Arg Pro His His	
675 680 685	
gat gct tct aca ttt acc ata aac att gca ctt aat aac gtg gga gaa	2112
Asp Ala Ser Thr Phe Thr Ile Asn Ile Ala Leu Asn Asn Val Gly Glu	
690 695 700	

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 705 710 715 720

gag tca cca cga aaa ggc tgg agc ttc atg cat cct ggg aga ctc aca 2208
 Glu Ser Pro Arg Lys Gly Trp Ser Phe Met His Pro Gly Arg Leu Thr
 725 730 735

cat ttgcatgaag gacttcctgt taaaaatgga acaagataca ttgcagtgtc 2261
 His

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 Ser Ile Pro Thr Asp Lys Leu Leu Val Ile Thr Val Ala Thr Lys Glu
 35 40 45
 Ser Asp Gly Phe His Arg Phe Met Gln Ser Ala Lys Tyr Phe Asn Tyr
 50 55 60
 Thr Val Lys Val Leu Gly Gln Gly Glu Glu Trp Arg Gly Gly Asp Gly
 65 70 75 80
 Ile Asn Ser Ile Gly Gly Gly Gln Lys Val Arg Leu Met Lys Glu Val
 85 90 95
 Met Glu His Tyr Ala Asp Gln Asp Asp Leu Val Val Met Phe Thr Glu
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 Cys Phe Asp Val Ile Phe Ala Gly Gly Pro Glu Glu Val Leu Lys Lys
 115 120 125

Phe Gln Lys Ala Asn His Lys Val Val Phe Ala Ala Asp Gly Ile Leu
130 135 140
Trp Pro Asp Lys Arg Leu Ala Asp Lys Tyr Pro Val Val His Ile Gly
145 150 155 160
Lys Arg Tyr Leu Asn Ser Gly Gly Phe Ile Gly Tyr Ala Pro Tyr Val
165 170 175
Asn Arg Ile Val Gln Gln Trp Asn Leu Gln Asp Asn Asp Asp Asp Gln
180 185 190
Leu Phe Tyr Thr Lys Val Tyr Ile Asp Pro Leu Lys Arg Glu Ala Ile
195 200 205
Asn Ile Thr Leu Asp His Lys Cys Lys Ile Phe Gln Thr Leu Asn Gly
210 215 220
Ala Val Asp Glu Val Val Leu Lys Phe Glu Asn Gly Lys Ala Arg Ala
225 230 235 240
Lys Asn Thr Phe Tyr Glu Thr Leu Pro Val Ala Ile Asn Gly Asn Gly
245 250 255
Pro Thr Lys Ile Leu Leu Asn Tyr Phe Gly Asn Tyr Val Pro Asn Ser
260 265 270
Trp Thr Gln Asp Asn Gly Cys Thr Leu Cys Glu Phe Asp Thr Val Asp
275 280 285
Leu Ser Ala Val Asp Val His Pro Asn Val Ser Ile Gly Val Phe Ile
290 295 300
Glu Gln Pro Thr Pro Phe Leu Pro Arg Phe Leu Asp Ile Leu Leu Thr
305 310 315 320
Leu Asp Tyr Pro Lys Glu Ala Leu Lys Leu Phe Ile His Asn Lys Glu
325 330 335
Val Tyr His Glu Lys Asp Ile Lys Val Phe Phe Asp Lys Ala Lys His
340 345 350
Glu Ile Lys Thr Ile Lys Ile Val Gly Pro Glu Glu Asn Leu Ser Gln
355 360 365
Ala Glu Ala Arg Asn Met Gly Met Asp Phe Cys Arg Gln Asp Glu Lys
370 375 380
Cys Asp Tyr Tyr Phe Ser Val Asp Ala Asp Val Val Leu Thr Asn Pro
385 390 395 400
Arg Thr Leu Lys Ile Leu Ile Glu Gln Asn Arg Lys Ile Ile Ala Pro
405 410 415
Leu Val Thr Arg His Gly Lys Leu Trp Ser Asn Phe Trp Gly Ala Leu
420 425 430

Ser Pro Asp Gly Tyr Tyr Ala Arg Ser Glu Asp Tyr Val Asp Ile Val
 435 440 445
 Gln Gly Asn Arg Val Gly Val Trp Asn Val Pro Tyr Met Ala Asn Val
 450 455 460
 Tyr Leu Ile Lys Gly Lys Thr Leu Arg Ser Glu Met Asn Glu Arg Asn
 465 470 475 480
 Tyr Phe Val Arg Asp Lys Leu Asp Pro Asp Met Ala Leu Cys Arg Asn
 485 490 495
 Ala Arg Glu Met Thr Leu Gln Arg Glu Lys Asp Ser Pro Thr Pro Glu
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 Thr Phe Gln Met Leu Ser Pro Pro Lys Gly Val Phe Met Tyr Ile Ser
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 Ser His Tyr Asn Asn Asp Leu Trp Gln Ile Phe Glu Asn Pro Val Asp
 545 550 555 560
 Trp Lys Glu Lys Tyr Ile Asn Arg Asp Tyr Ser Lys Ile Phe Thr Glu
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 Asn Ile Val Glu Gln Pro Cys Pro Asp Val Phe Trp Phe Pro Ile Phe
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 Ser Glu Lys Ala Cys Asp Glu Leu Val Glu Glu Met Glu His Tyr Gly
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 Lys Trp Ser Gly Gly Lys His His Asp Ser Arg Ile Ser Gly Gly Tyr
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 Glu Asn Val Pro Thr Asp Asp Ile His Met Lys Gln Val Asp Leu Glu
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 Asn Val Trp Leu His Phe Ile Arg Glu Phe Ile Ala Pro Val Thr Leu
 645 650 655
 Lys Val Phe Ala Gly Tyr Tyr Thr Lys Gly Phe Ala Leu Leu Asn Phe
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 Val Val Lys Tyr Ser Pro Glu Arg Gln Arg Ser Leu Arg Pro His His
 675 680 685
 Asp Ala Ser Thr Phe Thr Ile Asn Ile Ala Leu Asn Asn Val Gly Glu
 690 695 700
 Asp Phe Gln Gly Gly Gly Cys Lys Phe Leu Arg Tyr Asn Cys Ser Ile
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His

<210> 12

<211> 3718

<212> DNA

<213> Rattus rattus

<220>

<221> CDS

<222> (222)..(2486)

<400> 12

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ctgccgtccc gggccccacg tetaaccgg tgctcttcgg ggtctccgcg tctcgcgaga 180

agtcctcgcc gcaggcctcg ggctttcggg cttaggggcg g atg ggg gac cgc gga 236
Met Gly Asp Arg Gly
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gtg agg ctg ggg ctg ctg atg ccc atg ctc gcc ctg ctc tcc tgg gcg 284
Val Arg Leu Gly Leu Leu Met Pro Met Leu Ala Leu Leu Ser Trp Ala
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gct agc ctg ggc gta gcg gag gag act ccc tcg cgc atc cca gca gat 332
Ala Ser Leu Gly Val Ala Glu Glu Thr Pro Ser Arg Ile Pro Ala Asp
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aag tta tta gtc ata act gta gca acc aaa gaa aac gat gga ttc cac 380
Lys Leu Leu Val Ile Thr Val Ala Thr Lys Glu Asn Asp Gly Phe His
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Arg Phe Met Asn Ser Ala Lys Tyr Phe Asn Tyr Thr Val Lys Val Leu
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ggc caa ggg caa gag tgg aga ggt ggt gat ggg atg aac agt att gga 476
Gly Gln Gly Gln Glu Trp Arg Gly Gly Asp Gly Met Asn Ser Ile Gly
70 75 80 85

ggg ggc cag aag gtg aga tta atg aaa gaa gcc atg gag cac tac gcc 524

Gly	Gln	Asp	Asp	Leu	Val	Ile	Leu	Phe	Thr	Glu	Cys	Phe	Asp	Val	Ile		
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Phe	Ala	Gly	Gly	Pro	Glu	Glu	Leu	Leu	Lys	Lys	Phe	Gln	Lys	Thr	Asn		
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cat	aaa	atc	gtc	ttt	gca	gcg	gat	gcg	ctg	ttg	tgg	cca	gat	aag	cgg	668	
His	Lys	Ile	Val	Phe	Ala	Ala	Asp	Ala	Leu	Leu	Trp	Pro	Asp	Lys	Arg		
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Gln	Trp	Asp	Leu	Gln	Asp	Asn	Asp	Asp	Asp	Gln	Leu	Phe	Tyr	Thr	Lys		
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Val	Tyr	Ile	Asp	Pro	Leu	Lys	Arg	Glu	Ala	Leu	Asn	Ile	Thr	Leu	Asp		
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cac	aga	tgc	aaa	att	ttc	cag	gcc	ttg	aat	gga	gct	aca	gac	gaa	gtt	908	
His	Arg	Cys	Lys	Ile	Phe	Gln	Ala	Leu	Asn	Gly	Ala	Thr	Asp	Glu	Val		
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gaa	aca	ctg	cca	gtg	gcc	atc	aat	ggg	aat	ggg	ccc	acc	aaa	att	ctc	1004	
Glu	Thr	Leu	Pro	Val	Ala	Ile	Asn	Gly	Asn	Gly	Pro	Thr	Lys	Ile	Leu		
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Phe	Leu	Pro	Arg	Phe	Leu	Asp	Leu	Leu	Leu	Thr	Leu	Asp	Tyr	Pro	Lys		
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gaa	gca	ctt	cga	ctc	ttt	gtc	cat	aat	aaa	gaa	gtt	tat	cat	gaa	aag	1244	
Glu	Ala	Leu	Arg	Leu	Phe	Val	His	Asn	Lys	Glu	Val	Tyr	His	Glu	Lys		
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Asp Ile Lys Ala Phe Val Asp Lys Ala Lys His Asp Ile Ser Ser Ile	
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Lys Ile Val Gly Pro Glu Glu Asn Leu Ser Gln Ala Glu Ala Arg Asn	
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Met Gly Met Asp Phe Cys Arg Gln Asp Glu Lys Cys Asp Tyr Tyr Phe	
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Ser Val Asp Ala Asp Val Val Leu Thr Asn Pro Arg Thr Leu Lys Ile	
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Gly Lys Leu Trp Ser Asn Phe Trp Gly Ala Leu Ser Pro Asp Gly Tyr	
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Tyr Ala Arg Ser Glu Asp Tyr Val Asp Ile Val Gln Gly Asn Arg Val	
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Gly Ile Trp Asn Val Pro Tyr Met Ala Asn Val Tyr Leu Ile Gln Gly	
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Leu Gln Arg Glu Lys Asp Ser Pro Thr Pro Glu Thr Phe Gln Met Leu	
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Ser Pro Pro Lys Gly Val Phe Met Tyr Ile Ser Asn Arg His Glu Phe	
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Gly Arg Leu Ile Ser Thr Ala Asn Tyr Asn Thr Ser His Leu Asn Asn	
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Ile Asn Arg Asp Tyr Ser Lys Ile Phe Thr Glu Asn Ile Val Glu Gln	
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Lys His His Asp Ser Arg Ile Ser Gly Gly Tyr Glu Asn Val Pro Thr	
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Tyr Tyr Thr Lys Gly Phe Ala Leu Leu Asn Phe Val Val Lys Tyr Ser	
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Thr Ile Asn Ile Ala Leu Asn Asn Val Gly Glu Asp Phe Gln Gly Gly	
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Gly Cys Lys Phe Leu Arg Tyr Asn Cys Ser Ile Glu Ser Pro Arg Lys	
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ggc tgg agc ttc atg cat cct ggg agg ctt act cat cta cac gaa ggg	2444
Gly Trp Ser Phe Met His Pro Gly Arg Leu Thr His Leu His Glu Gly	
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Leu Pro Val Lys Asn Gly Thr Arg Tyr Ile Ala Val Ser Phe	
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<211> 755

<212> PRT

<213> Rattus rattus

<400> 13

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Thr	Val	Lys	Val	Leu	Gly	Gln	Gly	Gln	Glu	Trp	Arg	Gly	Gly	Asp	Gly		
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Cys	Phe	Asp	Val	Ile	Phe	Ala	Gly	Gly	Pro	Glu	Glu	Leu	Leu	Lys	Lys		
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Phe	Gln	Lys	Thr	Asn	His	Lys	Ile	Val	Phe	Ala	Ala	Asp	Ala	Leu	Leu		
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Trp	Pro	Asp	Lys	Arg	Leu	Ala	Asp	Lys	Tyr	Pro	Gly	Val	His	Ile	Gly		
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Lys	Arg	Tyr	Leu	Asn	Ser	Gly	Gly	Phe	Ile	Gly	Tyr	Ala	Pro	Tyr	Ile		
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Ser	Arg	Leu	Val	Gln	Gln	Trp	Asp	Leu	Gln	Asp	Asn	Asp	Asp	Asp	Gln		
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Leu	Phe	Tyr	Thr	Lys	Val	Tyr	Ile	Asp	Pro	Leu	Lys	Arg	Glu	Ala	Leu		
		195					200					205					
Asn	Ile	Thr	Leu	Asp	His	Arg	Cys	Lys	Ile	Phe	Gln	Ala	Leu	Asn	Gly		
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Pro	Thr	Lys	Ile	Leu	Leu	Asn	Tyr	Phe	Gly	Asn	Tyr	Val	Pro	Asn	Ser		
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Trp	Thr	Gln	Glu	Asn	Gly	Cys	Ala	Leu	Cys	Asp	Phe	Asp	Thr	Ile	Asp		
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	290					295					300						
Glu	Gln	Pro	Thr	Pro	Phe	Leu	Pro	Arg	Phe	Leu	Asp	Leu	Leu	Leu	Thr		
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Leu	Asp	Tyr	Pro	Lys	Glu	Ala	Leu	Arg	Leu	Phe	Val	His	Asn	Lys	Glu		
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Val	Tyr	His	Glu	Lys	Asp	Ile	Lys	Ala	Phe	Val	Asp	Lys	Ala	Lys	His		
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Ala Glu Ala Arg Asn Met Gly Met Asp Phe Cys Arg Gln Asp Glu Lys
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 Cys Asp Tyr Tyr Phe Ser Val Asp Ala Asp Val Val Leu Thr Asn Pro
 385 390 395 400
 Arg Thr Leu Lys Ile Leu Ile Glu Gln Asn Arg Lys Ile Ile Ala Pro
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 Ser Pro Asp Gly Tyr Tyr Ala Arg Ser Glu Asp Tyr Val Asp Ile Val
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 Gln Gly Asn Arg Val Gly Ile Trp Asn Val Pro Tyr Met Ala Asn Val
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 Tyr Leu Ile Gln Gly Lys Thr Leu Arg Ser Glu Met Ser Glu Arg Asn
 465 470 475 480
 Tyr Phe Val Arg Asp Lys Leu Asp Pro Asp Met Ser Leu Cys Arg Asn
 485 490 495
 Ala Arg Asp Met Thr Leu Gln Arg Glu Lys Asp Ser Pro Thr Pro Glu
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 Thr Phe Gln Met Leu Ser Pro Pro Lys Gly Val Phe Met Tyr Ile Ser
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 Ser His Leu Asn Asn Asp Leu Trp Gln Ile Phe Glu Asn Pro Val Asp
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 Trp Lys Glu Lys Tyr Ile Asn Arg Asp Tyr Ser Lys Ile Phe Thr Glu
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 580 585 590
 Ser Glu Arg Ala Cys Asp Glu Leu Val Glu Glu Met Glu His Tyr Gly
 595 600 605
 Lys Trp Ser Gly Gly Lys His His Asp Ser Arg Ile Ser Gly Gly Tyr
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 Glu Asn Val Pro Thr Asp Asp Ile His Met Lys Gln Ile Asp Leu Glu
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 Asn Val Trp Leu His Phe Ile Arg Glu Phe Ile Ala Pro Val Thr Leu
 645 650 655
 Lys Val Phe Ala Gly Tyr Tyr Thr Lys Gly Phe Ala Leu Leu Asn Phe
 660 665 670

Val Val Lys Tyr Ser Pro Glu Arg Gln Arg Ser Leu Arg Pro His His
675 680 685

Asp Ala Ser Thr Phe Thr Ile Asn Ile Ala Leu Asn Asn Val Gly Glu
690 695 700

Asp Phe Gln Gly Gly Gly Cys Lys Phe Leu Arg Tyr Asn Cys Ser Ile
705 710 715 720

Glu Ser Pro Arg Lys Gly Trp Ser Phe Met His Pro Gly Arg Leu Thr
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His Leu His Glu Gly Leu Pro Val Lys Asn Gly Thr Arg Tyr Ile Ala
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<210> 14

<211> 1486

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(396)

<400> 14

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His Gly Glu Gly Gly Gly Glu Glu Ala Ala Ala Ala Arg Glu Arg
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35 40 45

atc ttc ggc tgc tcc gag tgc gag aag ctg ttc cgc tca ccg cga gac 192
Ile Phe Gly Cys Ser Glu Cys Glu Lys Leu Phe Arg Ser Pro Arg Asp
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Leu Glu Arg His Val Leu Val His Thr Gly Glu Lys Pro Phe Pro Cys

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Leu Glu Cys Gly Lys Phe Phe Arg His Glu Cys Tyr Leu Lys Arg His				
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cga ctg ctg cac ggc acc gag cgg ccc ttc cct tgc cac atc tgc ggc				336
Arg Leu Leu His Gly Thr Glu Arg Pro Phe Pro Cys His Ile Cys Gly				
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aag ggc ttc atc acg ctc agc aac ctc tcc agg cac ctg aag ctg cac				384
Lys Gly Phe Ile Thr Leu Ser Asn Leu Ser Arg His Leu Lys Leu His				
	115	120	125	
cgg ggc atg gac tgactgccag gctgcgtgcg ccctgccctc caccagcct				436
Arg Gly Met Asp				
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<211> 132

<212> PRT

<213> Homo sapiens

<400> 15

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His Gly Glu Gly Gly Gly Glu Glu Ala Ala Ala Ala Arg Glu Arg
20 25 30

Gly Ser Ala Ser Gly Glu Pro Pro Ser Gly Ser Gly Arg Gly Lys Lys
35 40 45

Ile Phe Gly Cys Ser Glu Cys Glu Lys Leu Phe Arg Ser Pro Arg Asp
50 55 60

Leu Glu Arg His Val Leu Val His Thr Gly Glu Lys Pro Phe Pro Cys
65 70 75 80

Leu Glu Cys Gly Lys Phe Phe Arg His Glu Cys Tyr Leu Lys Arg His
85 90 95

Arg Leu Leu His Gly Thr Glu Arg Pro Phe Pro Cys His Ile Cys Gly
100 105 110

Lys Gly Phe Ile Thr Leu Ser Asn Leu Ser Arg His Leu Lys Leu His
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Arg Gly Met Asp
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<211> 580

<212> DNA

<213> Homo sapiens

<400> 16

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<213> Homo sapiens

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Met Lys Ala Gln Gly Leu Ser Phe Ser Phe Gln Arg Ala Pro Leu Ile
          20           25           30

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Phe His Arg Gln Phe Leu Leu Gln Gly Arg Leu Asn Gln Ala Lys Ile
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Asn Thr His Trp Tyr Thr Trp Leu Pro Thr Asn Phe Ile Cys Ile Tyr
          50           55           60

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Ile Phe Tyr Phe Gln His Pro His Ser Ser Trp Phe Asn Gln Ser Leu
65           70           75           80

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Val Leu Ala Asn Asn Lys Leu Val Arg Arg Ser Lys Val Val Asp Val
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Cys Thr Trp Leu Pro Trp Arg Ser Ser Gly Asp Ser Leu Phe Gln Asn
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Pro Phe Cys Thr Arg Trp Leu Leu
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<210> 18

<211> 4342

<212> DNA

<213> Homo sapiens

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<212> DNA

<213> Homo sapiens

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gcaaatgggg	tattcttcaa	agctccttct	ttttttaaat	cttcaaaggc	aattattctg	240
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<213> Artificial

<220>

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<400> 20

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<210> 21

<211> 551

<212> PRT

<213> Homo sapiens

<400> 21

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35 40 45
Pro Ser Asp Gly Leu Ser Asn Thr Glu Ser Ser Asp Gly Leu Asn Lys
50 55 60
Leu Leu Ala His Leu Leu Met Leu Ser Lys Arg Cys Pro Phe Lys Asp
65 70 75 80
Val Arg Glu Lys Ser Glu Phe Ile Leu Lys Ser Ile Gln Glu Leu Gly
85 90 95
Ile Arg Ile Pro Arg Pro Leu Gly Gln Gly Pro Ser Arg Phe Ile Pro
100 105 110
Glu Lys Glu Ile Leu Gln Val Gly Ser Glu Asp Ala Gln Met His Ala
115 120 125
Leu Phe Ala Asp Ser Phe Ala Ala Leu Gly Arg Leu Asp Asn Ile Thr
130 135 140
Leu Val Met Val Phe His Pro Gln Tyr Leu Glu Ser Phe Leu Lys Thr
145 150 155 160
Gln His Tyr Leu Leu Gln Met Asp Gly Pro Leu Pro Leu His Tyr Arg
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His Tyr Ile Gly Ile Met Ala Ala Ala Arg His Gln Cys Ser Tyr Leu
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Val Asn Leu His Val Asn Asp Phe Leu His Val Gly Gly Asp Pro Lys
195 200 205
Trp Leu Asn Gly Leu Glu Asn Ala Pro Gln Lys Leu Gln Asn Leu Gly
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Glu Leu Asn Lys Val Leu Ala His Arg Pro Trp Leu Ile Thr Lys Glu
225 230 235 240
His Ile Glu Gly Leu Leu Lys Ala Glu Glu His Ser Trp Ser Leu Ala
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 Glu Lys Met Arg Gln Leu Gln Glu Cys Arg Asp Glu Glu Glu Ala Ser
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